

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 29, 2002, 20:57:22 ; Search time 1530 Seconds
(without alignments)
273.912 Million cell updates/sec

Title: US-09-432-546-15
Sequence: 1 agagatgcttgcttgcttgctgaatgctcttatt 39

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estcom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gp_estl:*
11: gp_estl2:*
12: gp_hic:*
13: gp_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pin:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24.4	62.6	562	10	AW934005 EST359848
2	24.4	61.5	395	11	BG003920 MR3-GN018
3	23.8	61.0	282	11	W33571 mc54a10.r1
4	23.8	61.0	434	10	AA794057 v137f06.r
5	23.8	61.0	492	11	BE863099 UI-M-BHO-
6	23.8	61.0	535	11	BF383483 602045165
7	23.8	61.0	786	11	BG966767 602834644
8	23.8	61.0	963	11	W33574 mc54a10.r1
9	23.8	61.0	978	11	BI408490 602963270
10	23.2	59.5	606	11	BF497811 AT1211.5
11	23.2	59.5	609	11	BF499515 AT14081.5
12	23.2	59.5	1101	13	CNS00008 AL076628 Drosophila

13	22.8	58.5	668	10	AW081473
14	22.4	57.4	130	10	AW372361 PM4-BT034
15	22.4	57.4	137	10	AW372352 PM4-BT034
16	22.4	57.4	208	11	H47668 yf75b01.r1
17	22.4	57.4	245	10	AW373822 QY3-BT053
18	22.4	57.4	248	11	T20037 B300F Heart
19	22.4	57.4	251	10	AW373815 QV3-BT053
20	22.4	57.4	286	10	AW1756174 EESTea40
21	22.4	57.4	349	10	AA084811 zn02b12.s
22	22.4	57.4	361	11	BF733930 PM2-AN008
23	22.4	57.4	397	10	AA307345 EST178239
24	22.4	57.4	414	11	BE831169 PM4-MT003
25	22.4	57.4	436	10	BE780918 601469551
26	22.4	57.4	468	10	AA459606 zxr89604.r
27	22.4	57.4	472	10	BE047641 t239g08.y
28	22.4	57.4	496	10	AW328239 ds01b08.x
29	22.4	57.4	502	10	AA429048 zv33812.r
30	22.4	57.4	516	10	BE369822 601284323
31	22.4	57.4	526	10	BE549061 601070019
32	22.4	57.4	528	13	AO373589 RPC11.1-4
33	22.4	57.4	532	13	AO360666 HS_5034.7
34	22.4	57.4	542	10	AA314100 EST185950
35	22.4	57.4	561	10	AA130902 z014b05.r
36	22.4	57.4	565	13	AO405797 HS_5081.A
37	22.4	57.4	587	10	AA436939 zv72c04.r
38	22.4	57.4	600	10	BE391040 601285652
39	22.4	57.4	601	11	BG395154 602457640
40	22.4	57.4	605	10	AA075814 zv75d07.r
41	22.4	57.4	612	10	BE363428 601298386
42	22.4	57.4	613	10	BE255445 601116507
43	22.4	57.4	622	11	BG475162 602491717
44	22.4	57.4	624	11	BG707668 602670559
45	22.4	57.4	630	11	BG759481 602712037

ALIGNMENTS

RESULT 1
AW934005 562 bp mRNA EST 18-MAY-2001
LOCUS EST359848 tomato fruit mature green, TAMU Lycopersicon esculentum
DEFINITION cDNA clone cLEF57M14 5', mRNA sequence.
ACCESSION AW934005
VERSION AW934005.1 GI:8109406
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 562)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Rongling,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.
Location/Qualifiers
1..562
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF57M14"
/clone_id="tomato fruit mature green, TAMU"
/tissue-type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"

BASE COUNT	154 a	89 c	125 g	194 t
ORIGIN				
Query Match	62.6%	Score 24.4	DB 10	Length 562
Best Local Similarity	82.4%	Pred. No. 1.1e+02		
Matches 28	Conservative 0	Mismatches 6	Indels 0	Gaps 0
QY	5 gatggccttgatggcgcttggaatggccctctat 38			
Db	260 GATTTTATTGGTGCGCTTCGGAATAGCCCTTGT 293			
RESULT 2				
LOCUS	BG003920	395 bp	mRNA	EST 24-JAN-2001
DEFINITION	MRJ-GN0186-201100-011-809 GN0186 Homo sapiens CDNA, mRNA sequence.			
ACCESSION	BG003920			
VERSION	BG003920.1 GI:12444652			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 395) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. F., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. J., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.			
- TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	2002663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&t2=MR3-GN0186-201100-011-809&t3=2000-11-20&t4=1) Seq primer: puc 18 forward High quality sequence start: 5 High quality sequence stop: 395. Location/Qualifiers 1..395 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_1ib="GN0186" /dev_stage="Adult" /note="Organ: placenta;normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
FEATURES				
SOURCE				
BASE COUNT	93 a	118 c	111 g	73 t
ORIGIN				

Query Match	Best Local Similarity	Matches	Score	DB	Length
Query Match	84.4%	27	Score 24.1	DB 11	Length 395
Best Local Similarity	80.0%	28	Pred. No. 1.7e+02		
Matches	0	0	Mismatches	5	Indels
					Gaps
					0
					0

Query Match	Best Local Similarity	Matches	Score	DB	Length
Query Match	80.0%	28	Score 23.8	DB 11	Length 282
Best Local Similarity	80.0%	28	Pred. No. 1.7e+02		
Matches	0	0	Mismatches	7	Indels
					Gaps
					0
					0

DB	167	AGGACTGGCGCTTGGTTGCCTGGGAAGAGGCCACT	133
RESULT	4		
LOCUS	AA794057/c		
DEFINITION	AA794057	434 bp	mRNA
ACCESSION	VJ77f06.1	Barstead mouse myotubes MFLRB5	Mus musculus cDNA clone
VERSION	AA794057	IMAGE:1122851	5' mRNA sequence.
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	I (bases 1 to 434)		
JOURNAL	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubugue,T.,		
COMMENT	Geisel,S., Kucab,J., Lacy,M., Le,M., Martin,J., Morris,M.,		
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,		
	Thaising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and		
	Waterston,K.		
	The WashU-HMI Mouse EST Project		
	Unpublished (1996)		
	Contact: Marra M/Mouse EST Project		
	WashU-HMI Mouse EST Project		
	Washington University School of MedicineP		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: mouseest@watson.wustl.edu		
	This clone is available royalty-free through INLNL ; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	MG1:612187		
	Seq primer:-28m13 rev2 ET from Amersham		
	High quality sequence stop: 424.		
FEATURES	Location/Qualifiers		
SOURCE	1..434		
	/organism="Mus musculus"		
	/strain="C3H"		
	/db_xref="taxon:10090"		
	/clone_image="1122851"		
	/clone_id="Barstead mouse myotubes MFLRB5"		
	/cell_line="C2C12"		
	/lab_host="DH10B"		
	/note="Vector: pRTD-Pac (Pharmacia) with a modified		
	polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA		
	was primed with a Not I - oligo(dT) primer [5'		
	TGTTACGATCTGAAGTGAGCGAGCCGCCCTTTTTTTTTTTTTTTTTTTT		
	3'] double-stranded cDNA was ligated to Eco RI adaptors		
	(AATTGCACTCTGTG), digested with Not I and cloned into the		
	Not I and Eco RI sites of the modified pRTD vector.		
	Library constructed by Bob Barstead. The C2C12 cell line		
	(available from ATCC, catalog # CRL-1772) differentiates		
	rapidly, forming contractile myotubes and producing		
	characteristic muscle proteins."		
BASE COUNT	86 a	142 c	109 g
ORIGIN			97 t

	Query Match	Best Local Similarity	80.0%;	Pred.	No. 1,7e+02;	Mismatches	7;	Indels	0;
	Matches	28;	Conservative	0;	Gaps	0;			
Oy	1 aggagatgccttggtgccttgaatatgcctc	35							
Db	237 AGGACCTGGCCTTGGTTGCCTCGAAGGCCACT	203							

RESULT 5
BE863099/c BE863099 492 bp mRNA EST 29-SEP-2000 LOCUS

DEFINITION	UT-M-BH0-ajj-e-09-0-0-UI.11 NTH. BMAP_M.S1 Mus musculus cDNA clone
ACCESSION	UT-M-BH0-ajj-e-09-0-0-UI 5', mRNA sequence.
VERSION	BE863099
KEYWORDS	BE863099.1 GI:10382729
SOURCE	EST.
ORGANISM	house mouse.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
TITLE	1 (bases 1 to 492)
JOURNAL	Bonaldi,M.F., Lennon,G. and Soares,M.B.
MEDLINE	Normalization and subtraction: two approaches to facilitate gene
COMMENT	discovery Genome Res. 6 (9), 791-806 (1996) 97044477 Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Email: MESTRemail.nih.gov cDNA Library Preparation: M.B. Soares lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements Seq primer: M13 Reverse. Location/Qualifiers 1..492

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FEATURES
SOURCE
Location/Qualifiers
1. 492
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH0-aj-e-09-0-UI"
/clone_lib="NIH_BMAP_M.S1"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker. Site.1: Not I; Site.2: Eco RI; The
NIH_BMAP_M.S1 library is a subtracted library derived from
a mixture of normalized libraries from ten regions of the
mouse brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus). The driver used for
subtraction consisted of a pool of 20,000 cDNA clones
obtained from non-normalized and normalized libraries of
these ten regions of the mouse brain."
BASE COUNT      112 a      163 c      118 g      99 t
ORIGIN
Query Match      61.0%; Score 23.8; DB 11; Length 492;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY      1 agagagatgccttgctgagccttggaagaagcctct 35
||||| ||| ||||| ||||| ||||| ||||| ||
DB      490 AGGAGCTGGGCTGTGCTGGGAGGAGGCGCACT 456

```

RESULT	6
BF383483/c	
LOCUS	
DEFINITION	535 bp mRNA
ACCESSION	602045155F1 NCT_CGAP_L19 Mus musculus cDNA clone IMAGE:4194352 5' ,
VERSION	BF383483
KEYWORDS	BF383483.1 GI:11364788
SOURCE	EST.
ORGANISM	house mouse.
	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS      1 (bases 1 to 535)
TITLE        NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Jeffrey E. Green, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              DNA distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LHAM9528 row: b column: 17
              High quality sequence stop: 533.
              Location/Qualifiers
                1..535
                  /organism="Mus musculus"
                  /strain="FVB/N"
                  /db_xref="taxon:10090"
                  /clone="IMAGE:4194352"
                  /clone_1fb="NCI_CGAP_L19"
                  /lab_host="DH10B (T1 phage-resistant)"
                  /note="Organ: liver; Vector: pCMV-Sport6; Site.1: NotI;
                  Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                  Average insert size 1.9 kb. Constructed by Life
                  Technologies. Note: this is a NCI_CGAP Library."
                108 a 182 c 131 g 113 t 1 others

BASE COUNT
ORIGIN
108 a 182 c 131 g 113 t 1 others

Query Match      61.0%; Score 23.8; DB 11; Length 535;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0.

Oy 1 aggaatgaccttggtgccttggaatgcctct 35
    ||||| ||| ||||| ||||| ||||| ||||| ||
Db 286 AGGACTGGGCTTGCTTGCTTGCGAAGAGGCCACT 252

RESULT 7
LOCUS      BG966767/c
DEFINITION 602834644r1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4988986 5',
ACCESSION  BG966767
VERSION    BG966767.1 GI:14354404
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 786)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM11002 row: h column: 11
            High quality sequence start: 6
            High quality sequence stop: 779.
            Location/Qualifiers
              1..786
                /organism="Mus musculus"
                /strain="FVB/N"
                /db_xref="taxon:10090"

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/clone="IMAGE:4988986"
/clone_lib="NCI CGAP Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; PCMV-SpORT6; Site:1; NotI;
Site_2: SalI; Cloned unidirectionally.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT      170 a      264 c      195 g      157 t
ORIGIN
Query Match      61.0%; Score 23.8; DB 11; Length 786;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy      1 aggaatgacctgtgtgccttgaaatgaatgccttc 35
      ||||| ||| ||||| ||| ||| ||| ||| ||| |||
Db      556 AGGACCTGGGCTTGCTTGCCTGGGAAGAGGCCACT 522

RESULT      8
W33574      963 bp      mRNA      EST      13-MAY-1996
LOCUS      mc4b10.r1 Soares mouse embryo NBMEJ3.5 14.5 Mus musculus cDNA
DEFINITION      clone IMAGE:352315 5', mRNA sequence.
ACCESSION      W33574
VERSION      W33574.1 GI:1315625
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus.
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE      1 (bases 1 to 963)
AUTHORS      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
      Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
      Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
      Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
      Waterston,R.
TITLE      The WashU-HMNI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
      WashU-HMNI Mouse EST Project
      Washington University School of Medicine
      444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: mouseest@watson.wustl.edu
      This clone is available royalty-free through LNLN; contact the
      IMAGE Consortium (info@image.llnl.gov) for further information.
      MGI:224115
      Seq primer: ETPRimer
      High quality sequence stop: 321.
      Location/Qualifiers
          1..963
             /organism="Mus musculus"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="IMAGE:352315"
             /clone_lib="Soares mouse embryo NBMEJ3.5 14.5"
             /sex="unknown"
             /tissue_type="embryo"
             /dev_stage="13.5-14.5dpc total fetus"
             /lab_host="DH10B"
             /note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site:1; Not I; Site:2; Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15',
TGTTACCAATCTGACGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 j]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pRT3 vector. Library went through one round of

```

BASE COUNT	223 a	224 c	261 g	246 t	9 others
ORIGIN	normalization, and was constructed by Bento Soares and M. Fatima Bonaldó.				

Query Match	61.0%;	Score 23.8;	DB 11;	Length 963;
Best Local Similarity	80.0%;	Pred. No. 1.8e+02;		
Matches 28; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

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qy      1 aggagatgacctgtgtgccttgaataatgacctc 35
          ||||| ||| ||||| ||| ||| ||| ||
Db      167 AGGAGCTGGGCTTGTTGCTGGGAAGAGGCCACT 133

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RESULT	9
B1408490/c	
LOCUS	
DEFINITION	
BI408490	978 bp mRNA
602963270f1 NC1_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5118857	EST 14-AUG-2001
mRNA sequence.	
BI408490	
BI408490.1 GI:15169413	
EST.	
house mouse.	
SOURCE	
ORIGIN	

REFERENCE	AUTHORS	JOURNAL	COMMENT
1 (bases 1 to 978)	NIH-MGC	http://mgc.ncl.nih.gov/	
1 (bases 1 to 978)	National Institutes of Health	Mammalian Gene Collection (MGC)	
Unpublished (1999)	Contact: Robert Strausberg	Ph.D.	

tissue procurement: Gilbert Smith, Ph.D.
 cDNA library preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA library arrayed by: The I.M.A.G.E. consortium (LMNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
 plate: LMNL1289 row: k column: 18
 high quality sequence start: 4
 high quality sequence stop: 917.

FEATURES	Location/Qualifiers
source	1. .978

```

/organism="Mus musculus"
/strain="Czech 11"
/db_xref="taxon:10090"
/clone_1ib="IMAGE:511857"
/clone_1ib="NCI.CGAP.Lu33"
/tissue.type="pooled_lung_tumors"
/lab.host="DH10b (phage-resistant)"
/notes="Organ: lung; Vector: pTRIS-Pac (pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - o19o(47) primer [5', TGTTCCAACTGTGAAGTGGAGGCGGCCCTCTCTTTTATTTTATTTT 3'] . Double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

```

Query Match	61.0%;	Score 23.8;	DB 11;	Length 978;
Best Local Similarity	80.0%;	Pred. No. 1.8e+02;		
Matches 28;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	1	aggaagatgccttgatgagccttgaaagcgcctct	35	

Db 124 AGGAGCTGGGCTTGGTTGCCCTGGGAAGAGGCCACT 90

RESULT 10	LOCUS	DEFINITION
BF497811/c	606 bp	EST
BF497811	606 bp	EST
AF12111.5	prime AT	Drosophila melanogaster adult testes P0TB7

ACCESSION	BF497811	accession
VERSION	BF497811.2	version
KEYWORDS	GI:13689723	keywords
SOURCE	EST.	source
	fruit fly.	

REFERENCE
AUTHORS

Stapleton, M., Brocksstein, P., Hong, L., Agbayani, A., Baxter, E., Berman

TITLE
JOURNAL
COMMENT
Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11581112
Contact: Stapleton, M.
BPCB

Lawrence Berkeley National Lab
One Cyclotron Rd., Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/BST_est@fruitfly.berkeley.edu
hit genomic AEO03533: arm:3L [14543825,14818409]
estimated-cyto:70E7-71A2: 04/09/2001
Plate: AT.121 row: A column: 11
High quality sequence stop: 549.
location/Qualifiers
1..606
FEATURES
source

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/clone_lib="Arr Drosophila melanogaster adult testes potb7"
/sex="male"
/dev_stage="0-3 day old Ore-R males"
/lab_host="Plates Arr.10-Arr.120: DH5-alpha. Plates
Arr.121-Arr.319: DH5-alpha Tona"
/note="Organ: ADULT testes; Vector: potb7; Site.1: EcoRI;
Site.2: XhoI; The mRNA for the testis library was made
from testes and seminal vesicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into potb7. Plasmid cDNA library."

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Best local Similarity	89.3%	Pred. No. 2.8e+02;		
Matches	25; Conservative	0; Mismatches	3;	Indels 0; Gaps 0.
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Db	600	gagccttgaggccttcacgcgaatggccctc	573	

RESULT	11
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DEFINITION	BF499515 609 bp mRNA EST 19-Apr-2001
ACCESSION	AT1081.5prime AT Drosophila melanogaster adult testes protein Drosophila melanogaster cDNA clone AT14081 5 similar to CG33472: BFan0013472 Located on: 3L 70F5-70F6; 04/09/2001, mRNA sequence BF499515

VERSION BF499515.2 GI:13691376
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidae; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 609)
 Stapleton, M., Brokstein, P., Hong, L., Agbayan, A., Baxter, E., Berman, R., Carlson, J., Chame, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frisbe, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Mitra, S., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin, G. M.
 BDGP/HHMI AT Drosophila EST Project
 TITLE Unpublished (2000)
 JOURNAL On Dec 6, 2000 this sequence version replaced gi:11582816.
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST/estefruitfly.berkeley.edu>
 hit genomic AEO03533: arm:3L [14543825,14818409]
 estimated-cyco:70E7-71A2: 04/09/2001
 Plate: AT.140 row: G column: 9
 High quality sequence stop: 581.
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 /sex="male"
 /dev_stage="0-3 day old Ore-R males"
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 BASE COUNT 157 a 155 c 186 g 111 t
 ORIGIN

Query Match 59.5%; Score 23.2; DB 11; Length 609;
 Best Local Similarity 89.3%; Pred. No. 2.8e+02;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 ggccttggtgcttggaatgacctct 35
 ||||||| ||| |||||||
 Db 602 ggccttggtgcttggaatgacctct 575

RESULT 12
 CDS00008/c 1101 bp DNA GSS 03-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
 DEFINITION BAC38619 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 AL076628
 AL076628.1 GI:4956105
 VERSION
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidae; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 Genoscope.
 TITLE Direct Submission

JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqlref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammotter in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2: cn bw sp, the same strain used for the library p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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 /note="end : TET3"
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 ORIGIN

Query Match 59.5%; Score 23.2; DB 13; Length 1101;
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 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 ggccttggtgcttggaatgacctct 35
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 Db 362 ggccttggtgcttggaatgacctct 335

RESULT 13
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 DEFINITION similar to gb:U24097 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1202 ALPHA CHAIN (HUMAN);, mRNA sequence.
 AM081473
 AM081473.1 GI:6036625
 VERSION
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 668)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps@emall.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNT at:
www-bio.llnl.gov/bdrip/image/image.html
 Seq primer: -40UP from GIBCO
 High quality sequence stop: 415.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:2585896"

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			Indels	0;
			Gaps	0;
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Search completed: January 29, 2002, 21:50:19
Job time: 3177 sec

Wed Jan 30 10:06:07 2002

us-09-432-546-15.rst

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